

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 5, 2001, 15:19:11 : Search time 60.22 Seconds

(without alignments)
465.497 Million cell updates/sec

Title: US-09-593-316-4

Sequence: 1 MNVKGKVTLSMLVSTIVV.....IKLVKSMQTKRYVNNV 368

Scoring table: BL0SUM62
Gapop 10.0 / Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2008	100.0	368	2	A44785
2	1717.5	85.5	371	2	A45883
3	1701	84.7	376	2	A56480
4	1524.5	75.9	371	2	I49698
5	1476.5	73.5	394	2	A34417
6	658	32.8	295	2	PC1120
7	656	32.7	353	1	A34933
8	626	31.2	347	2	JC6126
9	456	22.7	189	2	PC1168
10	453.5	22.6	189	2	PC1165
11	452.5	22.5	189	2	PC1173
12	450.5	22.4	189	2	PC1166
13	449.5	22.4	189	2	PC1169
14	449.5	22.4	189	2	PC1170
15	449.5	22.4	189	2	PC1171
16	447.5	22.3	189	2	PC1172
17	118	5.9	26	2	A39769
18	115.5	5.8	505	2	A32261
19	102.5	5.1	559	2	A4987
20	101.5	5.1	559	2	JC4223
21	97.5	4.9	324	2	I45145
22	97	4.8	3724	2	T18427
23	94.5	4.7	585	2	C70634
24	94.5	4.7	1418	2	T45467
25	94.5	4.7	1520	2	B82274
26	94.5	4.7	2410	1	J01948
27	94	4.7	278	2	F86679
28	94	4.7	865	2	E84718
29	93	4.6	408	2	H64513

30	92.5	4.6	1487	1	CGH06C	collagen alpha 1(I)
31	90	4.5	708	1	TVVPT4	large T antigen -
32	89.5	4.5	478	2	H64970	mannose-1-phosphat
33	89.5	4.5	2054	2	T07584	hypothetical prote
34	89	4.4	688	1	TVVPTJ	large T antigen -
35	89	4.4	1827	1	00HU	sucrose alpha-glu
36	88.5	4.4	288	1	CGH06C	collagen alpha 1(I)
37	88.5	4.4	478	2	A85831	mannose-1-phosphat
38	88.5	4.4	483	2	T05188	protein kinase f41
39	88.5	4.4	708	2	S53411	hypothetical prote
40	88.5	4.4	788	2	A71076	hypothetical prote
41	88.5	4.4	1419	2	A41182	collagen alpha 1(I)
42	88.5	4.4	1487	2	B41182	collagen alpha 1(I)
43	88	4.4	533	2	T41382	acetamidase - tiss
44	88	4.4	567	2	C64478	hypothetical prote
45	88	4.4	609	2	T14759	hypothetical prote

ALIGNMENTS

RESULT 1
A44785
N-acetyllactosamine 3-alpha-galactosyltransferase (EC 2.4.1.124) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 29-Sep-1993
C:Accession: A44785
R:Joziasse, D.H.; Shaper, J.H.; Van den Eljnden, D.H.; Van Tancu, A.J.; Shaper, N.L.
J. Biol. Chem. 264, 14290-14297, 1989
A:Title: Bovine alpha1-3-galactosyltransferase: isolation and characterization of a
A:Reference number: A44785; MUID:89340543
A:Accession: A44785
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-368 <J02>
A:Cross-references: GB:J04989; NID:q163123; PID:AAA30558.1; PID:q163124
A:Superfamily: histo-blood group I transferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match	100.0%	Score 2008	DB 2	Length 368
Best Local Similarity	100.0%	Pred. No. 6.4e-161		
Matches 368	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MNVKGKVTLSMLVSTIVVENEYHSFEGSLFWINPSRNPFGSSIQKGMILPMPNN	60	
DB	1	MNVKGKVTLSMLVSTIVVENEYHSFEGSLFWINPSRNPFGSSIQKGMILPMPNN	60	
QY	61	GVNEEDSDINEKEORNEDESKLSDMPNPKRPVVYTKKAPVYVEGTYNRAVDN	120	
DB	61	GVNEEDSDINEKEORNEDESKLSDMPNPKRPVVYTKKAPVYVEGTYNRAVDN	120	
QY	121	VYAKKRTVGLTVFVAVGYIEHYLFETTSANKRPMVAGPVYFYIMVDVSNMPLIFELGP	180	
DB	121	VYAKKRTVGLTVFVAVGYIEHYLFETTSANKRPMVAGPVYFYIMVDVSNMPLIFELGP	180	
QY	181	LRSEFVEKIKRPMODISMKMKKTIGENIVANIQHEDVPLFCMDVNPVDFDKRSVETIG	240	
DB	181	LRSEFVEKIKRPMODISMKMKKTIGENIVANIQHEDVPLFCMDVNPVDFDKRSVETIG	240	
QY	241	ESVADLQMMVYKADPNDDTYERKRKSAVYIRGEGDFYVNAIFEGSTQVQVINTQEGFK	300	
DB	241	ESVADLQMMVYKADPNDDTYERKRKSAVYIRGEGDFYVNAIFEGSTQVQVINTQEGFK	300	
QY	301	GLLKAKKNDIEAQWDESHLNKPYLNKPTKLSPEYQWDYHIGLPADIKIVKMSQTK	360	
DB	301	GLLKAKKNDIEAQWDESHLNKPYLNKPTKLSPEYQWDYHIGLPADIKIVKMSQTK	360	
QY	361	YVNVVNNV 368		
DB	361	YVNVVNNV 368		

RESULT 2

146983 alpha 1,3-galactosyltransferase - pig

C1Species: Sus scrofa domestica (domestic pig)

C1Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 29-Sep-1999

C1Accession: 146584

ImmunoGenetics 41, 101-105, 1995

A1Title: cDNA sequence and chromosome localization of pig alpha 1,3 galactosyltransferase

A1Reference number: 146583; MIMID:95104914

A1Accession: 146584

A1Status: preliminary; translated from GH/FML/DdbH

A1Molecule type: mRNA

A1Residues: 1-371 <STR>

A1Cross-references: GH:146152; NID:q642635; P108:AAA73558.1; P10:q642636

C1Genetics:

A1Gene: GGTA1

C1Superfamily: histo-blood group 1 transferase

Query Match 85.5%; Score 1717.5; DB 2; Length 371;

Best Local Similarity 84.1%; Pred. No. 1,66-136;

Matches 313; Conservative 40; Mismatches 24; Indels 5; Gaps 3;

DB 1 MNVKKVILSMILVSTVIVVWEYIHSPGSLFWINPSRNFEVGSSTIQKGMLEPWFNN 60

DB 1 MNVKKVILSMILVSTVIVVWEYIHSPGSLFWINPSRNFEVGSSTIQKGMLEPWFNN 59

DB 61 G YHEEEDINNEKEKORNEHDESKIKSEWENPEKREPVVMTKKKAPVWVECTYKA 116

DB 60 GHSHEEEDINNEKEKORNEHDESKIKSEWENPEKREPVVMTKKKAPVWVECTYKA 119

DB 117 VLNYYAKOKITVGLTVFAVGRYIEHTLEFEETLSANKHFWGHPVIFYIMVDVSRMPL 176

DB 120 VLNYYAKOKITVGLTVFAVGRYIEHTLEFEETLSANKHFWGHPVIFYIMVDVSRMPL 179

DB 177 EAGPSEFVEKIKPKRKWDISMMRKKTIGEHVAHIGHEVDFLECMVDYVPGDQKRY 236

DB 180 EAGPSEFVEKIKPKRKWDISMMRKKTIGEHVAHIGHEVDFLECMVDYVPGDQKRY 239

DB 237 EHGSEVADLQAMWKADPNDFYERKESAAVIFPGEDPYFHAALFGCTFGVANTQ 296

DB 240 EHGSEVADLQAMWKADPNDFYERKESAAVIFPGEDPYFHAALFGCTFGVANTQ 299

DB 297 ECPKGLIKDKKNDIEAGMDESHLNKPYLLNKTKLISPEYGMVHIGLPADIKLVKMS 356

DB 400 ECPKGLIKDKKNDIEAGMDESHLNKPYLLNKTKLISPEYGMVHIGLPADIKLVKMS 359

DB 457 QTKENVVRNNV 468

DB 460 QTKENVVRNNV 371

RESULT 4

N acetylglucosaminide alpha 1,3 galactosyltransferase (EC 2.4.1.151) - marmoset

C1Species: Callithrix sp.

C1Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999

C1Accession: A56480

ImmunoGenetics 4, 194-201, 1994

A1Title: Identifying the minimal size of catalytically active primate alpha 1,3 galactosyltransferase

A1Reference number: A56480; MIMID:9431837

A1Accession: A56480

A1Status: preliminary

A1Molecule type: mRNA

A1Residues: 1-376 <STR>

A1Cross-references: GH:S71333; NID:q554051; P108:AAA11587.1; P10:q554052

A1Title: authors translated the codon GTC for residue 251 as Ser

C1Superfamily: histo-blood group 1 transferase

C1Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 84.7%; Score 1701; DB 2; Length 376;

Best Local Similarity 81.9%; Pred. No. 3,96-145;

Matches 308; Conservative 33; Mismatches 27; Indels 8; Gaps 2;

DB 1 MNVKKVILSMILVSTVIVVWEYIHSPGSLFWINPSRNFEVGSSTIQKGMLEPWFNN 60

DB 1 MNVKKVILSMILVSTVIVVWEYIHSPGSLFWINPSRNFEVGSSTIQKGMLEPWFNN 60

DB 61 GYH-----EHGDI-----NEKEQDNEDSKIKLSDMNIPKRPVAVMTKKKAPVWVECT 112

DB 61 GYH-----EHGDI-----NEKEQDNEDSKIKLSDMNIPKRPVAVMTKKKAPVWVECT 120

DB 113 YNPAIDNYYAKOKITVGLTVFAVGRYIEHTLEFEETLSANKHFWGHPVIFYIMVDVSR 172

DB 121 YNPAIDNYYAKOKITVGLTVFAVGRYIEHTLEFEETLSANKHFWGHPVIFYIMVDVSR 180

DB 173 MLELEGLIKSEKVKPKIKPKRKWDISMMRKKTIGEHVAHIGHEVDFLECMVDYVPGD 232

DB 181 APFTEIGPLRSFVFKVPEKRWQDISMMRKKTIGEHVAHIGHEVDFLECMVDYVPGD 240

DB 233 KPGVHTIGSEVADLQAMWKADPNDFYERKESAAVIFPGEDPYFHAALFGCTFGV 292

DB 241 HPGVHTIGSEVADLQAMWKADPNDFYERKESAAVIFPGEDPYFHAALFGCTFGV 300

DB 293 NITQETKGLIKDKKNDIEAGMDESHLNKPYLLNKTKLISPEYGMVHIGLPADIKLV 352

DB 401 NITQETKGLIKDKKNDIEAGMDESHLNKPYLLNKTKLISPEYGMVHIGLPADIKLV 360

DB 453 KMSWQTKENVVRNNV 368

DB 461 KMSWQTKENVVRNNV 376

RESULT 4

alpha 1,3-galactosyltransferase - mouse

C1Species: Mus musculus (house mouse)

C1Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999

C1Accession: 149698

ImmunoGenetics 4, 194-201, 1994

A1Title: Murine alpha 1,3-galactosyltransferase: A single gene locus specifies four 1

A1Reference number: A42117; MIMID:92184813

A1Accession: 149698

A1Status: preliminary; translated from GH/FML/DdbH

A1Molecule type: mRNA

A1Residues: 1-371 <RES>

A1Cross-references: GH:M85163; NID:q193563; P108:AAA3771.1; P10:q457142

C1Genetics:

A1Gene: gata-1

C1Superfamily: histo-blood group 1 transferase

Query Match 75.9%; Score 1524.5; DB 2; Length 371;

Best Local Similarity 73.6%; Pred. No. 2,50-120;

Matches 273; Conservative 44; Mismatches 51; Indels 4; Gaps 2;

DB 1 MNVKKVILSMILVSTVIVVWEYIHSPGSLFWINPSRNFEVGSSTIQKGMLEPWFNN 60

DB 1 MNVKKVILSMILVSTVIVVWEYIHSPGSLFWINPSRNFEVGSSTIQKGMLEPWFNN 60

DB 61 GYH-----EHGDI-----NEKEQDNEDSKIKLSDMNIPKRPVAVMTKKKAPVWVECT 112

DB 61 GYH-----EHGDI-----NEKEQDNEDSKIKLSDMNIPKRPVAVMTKKKAPVWVECT 120

DB 118 LUNYAKOKITVGLTVFAVGRYIEHTLEFEETLSANKHFWGHPVIFYIMVDVSRMPL 177

DB 121 LUNYAKOKITVGLTVFAVGRYIEHTLEFEETLSANKHFWGHPVIFYIMVDVSRMPL 180

DB 293 NITQETKGLIKDKKNDIEAGMDESHLNKPYLLNKTKLISPEYGMVHIGLPADIKLV 352

DB 401 NITQETKGLIKDKKNDIEAGMDESHLNKPYLLNKTKLISPEYGMVHIGLPADIKLV 360

DB 453 KMSWQTKENVVRNNV 368

DB 461 KMSWQTKENVVRNNV 376

A: Kofeleferron number: 121164; MUII: 93080551

A; Molecular Weight: 1000

A; Molecule type: DNA

A: Kreslunas: 1-1889 - KOM

† Superfamily: histo-blood group H transferase

Uncety Match 22.48, Score 449.5; DH 2; Length 1892

Host Local Similarity 46.5%; Pred. NO. 1.7e-10/
7.7. Minuteprob 74

Matches	87;	Conserved	27;	Mismatches	74;	Indels	1;	Gaps	1
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161 VILYIMOVSTRMPL,ELCTI,RSFKVFKI,KKKRWOD1SMRMKTI,GEHI,VAHIOHVIDP 220

2 WIIYVEFTIQTAAVPRVLTATTCOKI SVIACVAYKKRMOJDSMHMMI SDFOEKKRTLSVDY 61

221 LKCMVDYQVFKKFTVETLGHSSVAQLQMMYKADPNDFYERKKESAAVTFEGGDFYTH 280

6.2. IACVAVMEFKHGVVEILPLPGTLHPGFCSTREAFYFKRPOQAYIPKHGGFVYL 12

281 AA IGGTTOVINITTOETFKGILKDKKNDI PAQWHDESHINKYFLINKPDKLSPEYCWID 340

122 GPPGGVGEVQITRACHQAMVDQNGLEAVVHDSHLNKYLLRHKPTKVLSPETIMD 18

441 YII 101,13A 447

182 COLUMBIA 189

RECEIVED 1990

poly-
histo-blood group transferase - crab-eating macaque (*Fragment*)

et Species: Marcara fascicularis (crab-eating macaque)
et Date: 07-May-1993 #Structure_revision 07-May-1993 #text_change 07-May-1999